

Exhibit A

BLAST 2 SEQUENCES alignment of SEQ ID NO: 3 with 12ge20305orf30, a hypothetical *H. pylori* ORF disclosed by Smith et al. in WO 96/40893.



Blast 2 Sequences results

[PubMed](#)[Entrez](#)[BLAST](#)[OMIM](#)[Taxonomy](#)[Structure](#)

BLAST 2 SEQUENCES RESULTS VERSION BLASTN 2.2.10 [Oct-19-2004]

Match: Mismatch: gap open: gap extension:
x_dropoff: expect: wordsize: Filter Align

Sequence 1 lcl|seq_1 **Length** 759 (1 .. 759)

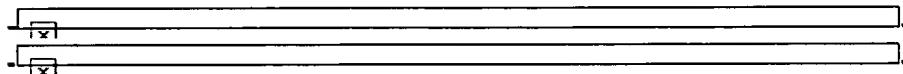
Sequence 2 lcl|seq_2 **Length** 768 (1 .. 768)



NOTE: The statistics (bitscore and expect value) is calculated based on the size of nr database

NOTE: If protein translation is reversed, please repeat the search with reverse strand of the query sequence

Score = 1344 bits (699), Expect = 0.0
Identities = 737/756 (97%)
Strand = Plus / Plus



Query: 1 atggcatacaaatatgatagagacttggaaattttaaagcaatttggaaatctagtgttta
60
Sbjct: 10 atggcatacaaatatgatagagacttggaaattttaaagcaacttggaaatctagtgttta
69

Query: 61 ttggatttgggggtgtttttggtaaagacggcgaaaaaagacacaatgaaaaa
120
Sbjct: 70 ttggatttgggggtgtttttggtaaagacggcgaaaaaagacacaatgaaaaa
129

Query: 121 ctgaccagctccatagaatacacaaggatggcgatgattacgctaaatacgcagaaaga
180

Sbjct: 130 ctcacaagctccatagaatacacaaaaggcatggcgatgattacgctaaatacgcagaaaga
189

Query: 181 atcgctgaagagttgcaatactatggagcaatagtttgcagttcattaaaggcgaa
240

Sbjct: 190 atcgctgaagagttgcaatactatggagcaatagtttgcagttcattaaaggtaaa
249

Query: 241 ggagtcttatacaaagagatttatgcgtgtgcataaattaaaggtaattacaac
300

Sbjct: 250 ggagtcttatacaaagagatttatgcgtgtgcataaattaaaggtaattacaac
300

Query: 301 aagaaaactgaaacgacttaattgaacaaaacatgcttctaaaatcttagaaagaagt
360

Sbjct: 310 aagaaaactgaaacgacttaattgaacaaaacatgcttctaaaatcttagaaagaagc
368

Query: 361 ttggaagaaatggatgatgaagaagtgaaagaaatgtgcgtgaattatccataaaaaac
420

420 | ||||||| Sbjct: 370 ctagaagaaatggatgatgaagaagtgaaagaaatgtgcgtatgtccataaaaaac
425

Query: 421 acggacaattaaacagacaaggcctaagcgccgacttaacgctgtttaaaatgggg
180

Sbjct: 430 acggacaattgaacagacaaggccttaagcgccgcacttaacgctgttaaaatggga
128

Query: 481 ggttttaatcttatcaatttagctgtcattttgcgaatgcggtcgaaaaaccattcta
510

Sbjct: 490 ggcttaaatcttatcaatttagctgtcattgtgcgaatgcggttgcaaaaaccattcta
518

Query: 541 gggcgtggttatcgcttcgggcaatcaggtgcttacaagaactctgagcttttaaca
600

Sbjct: 550 gggcgtggttatcgctgcgggcaatcaagtgc ttacaagaactctgagcttttaaca

Query: 601 ggtcctgtggctggatcattacaggcgatggacagcgattgatattgcagggccggct
660

Sbjct: 610 ggccctgtggatcattacaggcgatggacagcgattgatattgcagggccggct
669

Query: 661 tataggtaaccataccggcatgcattgtggttgccactttacgcctaaaaacacagcaa
720

Sbjct: 670 tataggtaaccataccggcatgcattgtggtcgccacttacgcctaaaaacgcaaca
728

Query: 721 qccaatqqaqataagaagtcgttcaaataagaatcc 756

1 2 3 4 5 6 7 8 9 10 11 12 13 14 15 16 17 18 19 20 21 22 23 24 25 26 27 28 29 30 31 32 33 34 35 36 37 38 39 40 41 42 43 44 45 46 47 48 49 50 51 52 53 54 55 56 57 58 59 60 61 62 63 64 65 66 67 68 69 70 71 72 73 74 75 76 77 78 79 80 81 82 83 84 85 86 87 88 89 90 91 92 93 94 95 96 97 98 99 100

Sbjct: 730 qccaatqaaqataaqaagtcgttqcaaataagaatcc 765

CPU time: 0.02 user secs. 0.01 sys. secs 0.03 total secs.

Lambda	K	H
1.33	0.621	1.12

Gapped
Lambda K H
1.33 0.621 1.

```
Matrix: blastn matrix:1 -2
Gap Penalties: Existence: 5, Extension: 2
Number of Sequences: 1
Number of Hits to DB: 166
Number of extensions: 1
Number of successful extensions: 1
Number of sequences better than 10.0: 1
Number of HSP's better than 10.0 without gapping: 1
Number of HSP's gapped: 1
Number of HSP's successfully gapped: 1
Number of extra gapped extensions for HSPs above 10.0: 0
Length of query: 759
Length of database: 12,305,973,192
Length adjustment: 26
Effective length of query: 733
Effective length of database: 12,305,973,166
Effective search space: 9020278330678
Effective search space used: 9020278330678
Neighboring words threshold: 0
Window for multiple hits: 0
X1: 11 (21.1 bits)
X2: 26 (50.0 bits)
X3: 26 (50.0 bits)
S1: 12 (23.8 bits)
S2: 21 (41.1 bits)
```

CODING SEQUENCE WITH HOMOLOGY TO SEQ ID NO: 3 DISCLOSED BY
SMITH ET AL.

L1 ANSWER 1 OF 1 REGISTRY COPYRIGHT 2004 ACS on STN
RN 186778-60-9 REGISTRY
CN DNA (*Helicobacter pylori* strain J99 open reading frame
12ge20305orf30)
(9CI) (CA INDEX NAME)
FS NUCLEIC ACID SEQUENCE
SQL 768
NA 268 a 123 c 178 g 199 t
NTE doublestranded

SEQ 1 aggaataata tggcatacaa atatgataga gacttggaaat ttttaagca
51 acttggaaatct agtgattttt tggatttgtt cgaggtgctt gtttttggta
101 aagacggcga aaaaagacac aatgaaaaac tcacaagctc catagaatac
151 aaaaggcatg gcgatgatta cgctaaatac gcagaaagaa tcgctgaaga
201 gttgcaatac tatgggagca atagtttgc gagtttcatt aaaggtaag
251 gagtcttata caaagagatt ttatgcgatg tgtgcgataa attaaaggc
301 aattacaaca agaaaaactga aacgacttta attgaacaaa acatgcttc
351 taaaatctta gaaagaagcc tagaagaaat ggatgatgaa gaagtgaaag
401 aaatgtgcga tgaattgtcc ataaaaaaaca cggacaattt gaacagacaa
451 gccttaagcg cggcgacttt aacgctgttt aaaatgggag gctttaatc
501 ttatcaatta gctgtcattt ttcgcaatgc gtttgcacaaa accattctag
551 ggcgtggttt atcgcttgcg ggcaatcaag tgcttacaag aactctgagc
601 ttttaacag gccctgttgg ctggatcatt acaggcgtat ggacagcgtat
651 tgatattgca gggccggctt ataggtaac cataccggca tgcattgtgg
701 tcgcccacttt acgcctaaaa acgcaacaag ccaatgaaga taagaagtgc
751 ttgcaaatag aatccgtt

MF Unspecified
CI MAN
SR CA
LC STN Files: CA, CAPLUS, USPATFULL
DT.CA CAplus document type: Patent
RL.P Roles from patents: ANST (Analytical study); BIOL (Biological study);
PREP (Preparation); PRP (Properties); USES (Uses)
1 REFERENCES IN FILE CA (1907 TO DATE)
1 REFERENCES IN FILE CAPLUS (1907 TO DATE)

HP30 Coding Sequence, SEQ ID NO: 3

atggcatacaaataatgatagagacttggatTTTaaagcaattggaatcttagtgattta
ttggatttgggtttggatTTTggtaaagacggcgaaaaaaagacacaatggaaaaaa
ctgaccagctccatagaatacAAAaggcatggcgatgattacgctaaatacgcagaaaga
atcgctgaagagttgcaataactatggagcaatagtTTTgcgatTTTcattaaaggcgaa
ggagtcttatacaaagagatTTTatgcgatgtgcgatTTTaaaggcattacaac
aagaaaaactgaaacgactttaattgaacaaaacatgcTTTctaaaatcttagaaagaagt
ttggaaagaatggatgatgaagaagtggaaatgtgcgatgattatccataaaaaac
acggacaatttaaacagacaaggcTTTaaacgcggcgactttaaacgcgtttaaaatgggg
ggTTTaaatcttattcaatttagctgtcattgtgcgatgcggcgatTTTaaaaccattcta
ggcgtggTTTatcgcttgcggcaatcaggcgatggacagcgattgatattgcaggggcgct
tataggtaaccataccggcatgcattgtggccactttacgcctaaaaacacagcaa
gccaatggagataagaagtgcgttgcattacaatccatt